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Advanced proteomic approaches to identify and characterize of Lin28 molecular complexes regulating mRNA recognition and translation in embryonic stem cells.

The RNA-binding protein Lin28a is emerged as a crucial regulator of embryonic stem cell (ESC) differentiation as well as a key factor in the development of many tumors. The current idea is that Lin28a works by enhancing or blocking the translation of hundreds of mRNA targets. How Lin28 achieves this incredibly complex orchestration of its targets remains to be determined. In this project, we aim to understand in which way Lin28a fulfills these different regulation mechanisms by analyzing its protein interactome network and mRNA targets through enhanced proteomic approaches and massive mass spectrometry coupled with well-suited molecular biology experimental approaches in the model system of ESC differentiation into epiblast-like stem cells. The results will add new insights in the understanding of the molecular mechanisms of Lin28 functions in the regulation of mRNA availability for translation in stem cell differentiation.